



ENTERED 1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/720,383C

DATE: 03/27/2003 86

TIME: 12:40:52

Input Set : A:\BB-1170 Corrected Sequence Listing.txt

Output Set: N:\CRF4\03272003\I720383C.raw

RECEIVED

APR 01 2003

TECH CENTER 1600/2900

```

3 <110> APPLICANT: Stephen M. Allen
4   Gary M. Fader
5   Saverio Carl Falco
6   Anthony J. Kinney
7   Jonathan E. Lightner
8   Guo-Hua Miao
9   J. Antoni Rafalski
10  Catherine J. Thorpe
12 <120> TITLE OF INVENTION: Plant Cellulose Synthases
14 <130> FILE REFERENCE: BB-1170
16 <140> CURRENT APPLICATION NUMBER: 09/720,383C
17 <141> CURRENT FILING DATE: 2000-12-21
19 <150> PRIOR APPLICATION NUMBER: 60/092,844
20 <151> PRIOR FILING DATE: 1998-07-14
22 <160> NUMBER OF SEQ ID NOS: 29
24 <170> SOFTWARE: Microsoft Office 97
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1221
28 <212> TYPE: DNA
29 <213> ORGANISM: Hordeum vulgare
31 <400> SEQUENCE: 1
32 gcacgaggat attcttactg ggtttaaaaat gcacgcaaga ggttggatat caatctactg   60
33 catgccacca cgacctgtgt tcaaggggttc tgcgccaatc aatctctctg accgtctcaa   120
34 tcaagttctc cgggtgggctc ttgggtcagt tgaaattctg tttagcagac attgtcctat   180
35 ctggtacaat tacggtgggc ggttgaaact tctggagagg atggcttaca tcaacaccat   240
36 tgtttatcca ataacatccc ttccacttat cgcctattgt gtgcttcctg ctatctgtct   300
37 cctcaccaac aaatttatca ttcccagagat cagtaactat gctgggatgt tctttattct   360
38 tatgtttgcc tccatctttg ccacgggtat attggagctg cgatggagtg gtgtcggcat   420
39 cgaggactgg tggagaaaacg agcagttctg ggttattggt ggcacatctg cccatctttt   480
40 cgcagtgttc caggggtctgc tgaaggtgtt ggccgggatt gacaccaact tcacggttac   540
41 ctcgaaggca aacgacgagg atggcgattt tgctgagtta tacgtgttca agtggaccag   600
42 tctcctcatt cctccgacca ccgtccttgt gattaacctg gtgggcatgg tggcaggcat   660
43 atcatatgcc atcaacagcg gttaccagtc ttgggggtcca ctcttcggaa agctcttctt   720
44 ctcaatctgg gtgatcctcc atctctaccc ctctctcaag ggtctcatgg ggaagcagaa   780
45 ccgcacgcca accatcgta ttgtttggtc catcctccta gcctccatct tctccctcct   840
46 gtgggtgaag atcgaccctt tcatatccga taccagaaaa gccgtcgcca tggggcagtg   900
47 tggcgtaaac tgctgatcgg cgccgaagag tatctgcccc cctcgtgtaa ataccggagg   960
48 ggggttgatg ggattttgtt gttgtagatg aagacggagt tttatgtaag ttattattgc  1020
49 cccttcgtgc tgagaagcac aaaccgtgaa gcctacgaaa cctgcagcgt acattgtgat  1080
50 ttttttctcc ttttcttttc atctgtgata cctgttggtt cttcttagag tatattatgt  1140
51 cagaacgtat ctatagttct atacacacta tgacaccaac tatttatata aggcagctgt  1200
52 tgcatacaact cttctgcaaa a                                     1221
54 <210> SEQ ID NO: 2

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55 <211> LENGTH: 304
56 <212> TYPE: PRT
57 <213> ORGANISM: Hordeum vulgare
59 <400> SEQUENCE: 2
60 His Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly Trp Ile
61   1           5           10           15
63 Ser Ile Tyr Cys Met Pro Pro Arg Pro Cys Phe Lys Gly Ser Ala Pro
64           20           25           30
66 Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly
67           35           40           45
69 Ser Val Glu Ile Leu Phe Ser Arg His Cys Pro Ile Trp Tyr Asn Tyr
70           50           55           60
72 Gly Gly Arg Leu Lys Leu Leu Glu Arg Met Ala Tyr Ile Asn Thr Ile
73   65           70           75           80
75 Val Tyr Pro Ile Thr Ser Leu Pro Leu Ile Ala Tyr Cys Val Leu Pro
76           85           90           95
78 Ala Ile Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu Ile Ser Asn
79           100          105          110
81 Tyr Ala Gly Met Phe Phe Ile Leu Met Phe Ala Ser Ile Phe Ala Thr
82           115          120          125
84 Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Gly Ile Glu Asp Trp Trp
85           130          135          140
87 Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala His Leu Phe
88 145          150          155          160
90 Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp Thr Asn
91           165          170          175
93 Phe Thr Val Thr Ser Lys Ala Asn Asp Glu Asp Gly Asp Phe Ala Glu
94           180          185          190
96 Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro Thr Thr Val
97           195          200          205
99 Leu Val Ile Asn Leu Val Gly Met Val Ala Gly Ile Ser Tyr Ala Ile
100          210          215          220
102 Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe
103 225          230          235          240
105 Ser Ile Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys Gly Leu Met
106           245          250          255
108 Gly Lys Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu
109           260          265          270
111 Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Lys Ile Asp Pro Phe Ile
112           275          280          285
114 Ser Asp Thr Gln Lys Ala Val Ala Met Gly Gln Cys Gly Val Asn Cys
115          290          295          300
117 <210> SEQ ID NO: 3
118 <211> LENGTH: 3776
119 <212> TYPE: DNA
120 <213> ORGANISM: Zea mays
122 <400> SEQUENCE: 3
123 gcgcgccgcg caggcgcaac gcaacaaagg gaaaccccag ccggaggagc aaaagctagc 60
124 aagcgtgtcc ctcccctcc ctactcccg ttctattcca ttcccccca gacgccgcta 120

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125 cdgccgcgcg cgcacgcacg cttgcccccg gatctggaga tctggtagcg ccagggggat 180
126 ggaggccagc gccgggctgg tcgccggctc gcacaaccgg aacgagctcg tcgtcatccg 240
127 ccgcgatggc gagccagggc cgaagcccat ggaccagcgg aacggccagg tgtgccagat 300
128 ttgcggcgac gacgtggggc gcaaccccca cggggagccg ttcgtggcct gcaacgagt 360
129 cgccttcccc atctgccggg actgctacga gtacgagcgc cgcgagggca cgcagaact 420
130 cccccagtgc aagaccgcct tcaagcgcct caaggggtgc gcgcgcgtgc ccggggacga 480
131 ggaggaggac ggcgctgcag acctggagaa cgagttcaac tggagcgaca agcacgactc 540
132 ccagtacctc gccgagtcca tgctccacgc ccacatgagc tacggccgcg gcgccgacct 600
133 cgacggcgtg ccgcagccat tccaccccat cccaatggt cccctcctca ccaacggaca 660
134 gatggtcgat gacatcccg cggaccagca cgcccttgtg ccctcgttcg tgggtggcgg 720
135 gggaagagg attcaccctc tcccgtagc ggatcccaac ctctctgtgc aaccgaggtc 780
136 tatggaccct tccaaggatc tcgccgcata tggctacggg agcgtagcat ggaaggagag 840
137 gatggagagc tggaagcaga agcaggagag gatgcaccag acgaggaaac atggcggcgg 900
138 cgatgatggt gatgatgcag atctaccact aatggatgaa gctagacagc cattgtccag 960
139 aaagatcccg ctctcttcaa gccaaatcaa cccctatagg atgattataa taattcggct 1020
140 agtggttttg tgtttcttct tccactaccg agtgcagcat ccggtgcctg atgcatttgc 1080
141 ttatggctc atactctgta tctgtgaaat ttggtttgcc atgtcttggg ttcttgacca 1140
142 gtttccaaag tggtttccta tcgagaggga aacctatctt gaccggctga gtttaagggt 1200
143 tgacaaggaa gggcatcctt ctcaactcgc ccctgttgat ttctttgtca gtacggttga 1260
144 tcccttgaag gaacctccat tggctactgc taatactgtt ctatctatcc tttcggtgga 1320
145 ttatccagtt gataaggttt catgctacgt ttctgatgat ggtgctgcca tgctgacatt 1380
146 tgaagcattg tctgaaacat ctgaatttgc aaagaaatgg gttcctttct gcaaaagata 1440
147 tagccttgag cctcgtgctc cagagtggta ctccaacag aagatagact acctgaaaga 1500
148 caaggtggcg ccaaactttg ttagagaacg gagagcaatg aagagagagt atgaggaatt 1560
149 caaggtcaga atcaatgcct tggttgctaa agcccaaaag gttcctgagg aaggatggac 1620
150 aatgcaggat ggaactccat ggcccggaaa taatgtccgt gatcatcctg gaatgattca 1680
151 ggttttctct gtgcaaaagt gtggccatga tgtggaagga aatgagctgc ctcgatttgt 1740
152 ttatgtttca agagaaaaac ggccaggcta caaccatcac aagaaggctg gtgctatgaa 1800
153 tgcatgtgtc cgagtctctg ctgtactaac taatgtcctt tatttgcctga acttggtatt 1860
154 tgatcactat atcaataata gtaaggctat aaaggaagca atgtgtttta tgatggatcc 1920
155 tttgcttgga aagaaagttt gctatgtgca gtttccctca agatttgatg ggattgatcg 1980
156 ccatgatcga tatgctaaca gaaatgttgt ctttttcgat atcaacatga aaggtttgga 2040
157 tggtatccag ggcccaattt atgtgggtac tggatgtgtc ttcagaaggc aggcattata 2100
158 tggctacgat gtccccaaaa caaagaagcc accatcaaga acttgcaact gctggccaaa 2160
159 gtggtgcatt tgctgttgct gttttggtta caggaagacc aagaagaaga ccaagacctc 2220
160 taaacctaaa tttgagaaga taaagaaact ttttaagaaa aaggaaaatc aagccctgc 2280
161 atatgctctt ggtgaaattg atgaagccgc tccaggagct gaaaaagaaa aggctagtat 2340
162 tgtaaatcaa cagaagtttg aaaagaaatt tggccagtct tcagtttttg ttgcatccac 2400
163 acttcttgag aatggtggaa ccctgaagag tgccagtcca gcttctcttc tgaaggaagc 2460
164 tatacatgtc atcagttgtg gatatgaaga caaaacaggc tggggaaaag atattggttg 2520
165 gatttatgga tcagtcacag aagatattct tactgggttt aagatgcact gccatggttg 2580
166 gcggtcaatt tactgcatac ctaaaccggc cgcttcaaaa ggttccgcac ctctcaatct 2640
167 tccgatcgt ctccaccagg ttcttcggtg ggctcttggt tcaattgaaa ttttcttcag 2700
168 caaccactgc cctctctggt atgggtatgg tgggtggacta aagtctctgg aaaggttttc 2760
169 gtacattaac tccatcgat acccttgga atctatccc ctcttgccct attgcacatt 2820
170 gcctgccatc tgcttgctga cagggaatt tatcacgcca gagcttaaca atgttgccag 2880
171 cctctggttc atgtcactt tcatctgcat ttttgctacg agcatcctgg aaatgagatg 2940
172 gagtgggtga ggcatcgatg actggtggag aaacgagcag ttttgggtca ttggaggcgt 3000
173 gtcttcacat ctctttgctg tgttcaggg actcctcaag gtcatagctg gtgtagacac 3060

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174 gagcttcact gtgacatcca agggcgaggaga cgacgaggag ttctcagagc tgtacacatt 3120
175 caaatggacg acccttctga tacctccgac aacctgctc ctactgaact tcattggagt 3180
176 ggtagctggc atctccaatg cgatcaacaa cggatatgaa tcatggggcc ccctgttcgg 3240
177 gaagctcttc ttgtcatttt ggggtgatcgt ccattctttac ccgttcctca aggggtctgg 3300
178 tgggaggcag aacaggacgc caacgattgt cattgtctgg tccatcctcc tggcttcgat 3360
179 cttctcgctg ctttgggtcc ggatcgaccc gttccttgcg aaggatgatg gtcccctgtt 3420
180 ggaggagtgt ggtctggatt gcaactagga ggtcagcacg tggacttccc cgtcagtgtg 3480
181 tggtcgaaga agtatttttt cagatgtttt gtgccatat ttcttttttc aatttttgtc 3540
182 cctctgtaga tagaaacaag gggagaaggg gaaaaaaagt acttgtattt cttttgttcc 3600
183 atggtggtgg tgggtggtgg cggtcagcc tcgtgagtgc agtattgggc aaaccggagg 3660
184 ctgcggaac cttgtgcagt tcggccacga atatactagg gaagatcgcg accaatcaat 3720
185 caatcgatga ccgagttcaa ttgttcagca aaaaaaaaaa aaaaaaaaaa aaaaaa 3776

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187 <210> SEQ ID NO: 4

188 <211> LENGTH: 1148

189 <212> TYPE: PRT

190 <213> ORGANISM: Zea mays

192 <400> SEQUENCE: 4

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193 Arg Ala Ala Gln Ala Gln Arg Asn Lys Gly Lys Pro Gln Pro Glu Glu
194   1           5           10           15
196 Gln Lys Leu Ala Ser Val Ser Leu Pro Leu Pro His Ser Arg Phe Ile
197           20           25           30
199 Pro Phe Pro Pro Arg Arg Arg Tyr Arg Arg Arg Arg Thr His Ala Cys
200           35           40           45
202 Pro Gly Ile Trp Arg Ser Gly Ser Ala Arg Gly Met Glu Ala Ser Ala
203           50           55           60
205 Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu Leu Val Val Ile Arg
206   65           70           75           80
208 Arg Asp Gly Glu Pro Gly Pro Lys Pro Met Asp Gln Arg Asn Gly Gln
209           85           90           95
211 Val Cys Gln Ile Cys Gly Asp Asp Val Gly Arg Asn Pro Asp Gly Glu
212           100          105          110
214 Pro Phe Val Ala Cys Asn Glu Cys Ala Phe Pro Ile Cys Arg Asp Cys
215           115          120          125
217 Tyr Glu Tyr Glu Arg Arg Glu Gly Thr Gln Asn Cys Pro Gln Cys Lys
218           130          135          140
220 Thr Arg Phe Lys Arg Leu Lys Gly Cys Ala Arg Val Pro Gly Asp Glu
221 145           150          155          160
223 Glu Glu Asp Gly Val Asp Asp Leu Glu Asn Glu Phe Asn Trp Ser Asp
224           165          170          175
226 Lys His Asp Ser Gln Tyr Leu Ala Glu Ser Met Leu His Ala His Met
227           180          185          190
229 Ser Tyr Gly Arg Gly Ala Asp Leu Asp Gly Val Pro Gln Pro Phe His
230           195          200          205
232 Pro Ile Pro Asn Val Pro Leu Leu Thr Asn Gly Gln Met Val Asp Asp
233           210          215          220
235 Ile Pro Pro Asp Gln His Ala Leu Val Pro Ser Phe Val Gly Gly Gly
236 225           230          235          240
238 Gly Lys Arg Ile His Pro Leu Pro Tyr Ala Asp Pro Asn Leu Pro Val
239           245          250          255

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241 Gln Pro Arg Ser Met Asp Pro Ser Lys Asp Leu Ala Ala Tyr Gly Tyr
242                260                265                270
244 Gly Ser Val Ala Trp Lys Glu Arg Met Glu Ser Trp Lys Gln Lys Gln
245                275                280                285
247 Glu Arg Met His Gln Thr Arg Asn Asp Gly Gly Gly Asp Asp Gly Asp
248                290                295                300
250 Asp Ala Asp Leu Pro Leu Met Asp Glu Ala Arg Gln Pro Leu Ser Arg
251 305                310                315                320
253 Lys Ile Pro Leu Pro Ser Ser Gln Ile Asn Pro Tyr Arg Met Ile Ile
254                325                330                335
256 Ile Ile Arg Leu Val Val Leu Cys Phe Phe Phe His Tyr Arg Val Met
257                340                345                350
259 His Pro Val Pro Asp Ala Phe Ala Leu Trp Leu Ile Ser Val Ile Cys
260                355                360                365
262 Glu Ile Trp Phe Ala Met Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp
263                370                375                380
265 Phe Pro Ile Glu Arg Glu Thr Tyr Leu Asp Arg Leu Ser Leu Arg Phe
266 385                390                395                400
268 Asp Lys Glu Gly His Pro Ser Gln Leu Ala Pro Val Asp Phe Phe Val
269                405                410                415
271 Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Val Thr Ala Asn Thr
272                420                425                430
274 Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp Lys Val Ser Cys
275                435                440                445
277 Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Glu Ala Leu Ser
278                450                455                460
280 Glu Thr Ser Glu Phe Ala Lys Lys Trp Val Pro Phe Cys Lys Arg Tyr
281 465                470                475                480
283 Ser Leu Glu Pro Arg Ala Pro Glu Trp Tyr Phe Gln Gln Lys Ile Asp
284                485                490                495
286 Tyr Leu Lys Asp Lys Val Ala Pro Asn Phe Val Arg Glu Arg Arg Ala
287                500                505                510
289 Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn Ala Leu Val
290                515                520                525
292 Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Gln Asp Gly
293                530                535                540
295 Thr Pro Trp Pro Gly Asn Asn Val Arg Asp His Pro Gly Met Ile Gln
296 545                550                555                560
298 Val Phe Leu Gly Gln Ser Gly Gly His Asp Val Glu Gly Asn Glu Leu
299                565                570                575
301 Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Tyr Asn His
302                580                585                590
304 His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala Val
305                595                600                605
307 Leu Thr Asn Ala Pro Tyr Leu Leu Asn Leu Asp Cys Asp His Tyr Ile
308                610                615                620
310 Asn Asn Ser Lys Ala Ile Lys Glu Ala Met Cys Phe Met Met Asp Pro
311 625                630                635                640
313 Leu Leu Gly Lys Lys Val Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/27/2003
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:14; Xaa Pos. 201
Seq#:19; N Pos. 262
Seq#:20; Xaa Pos. 88

VERIFICATION SUMMARY

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L:1292 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:192

L:1844 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:240

L:1896 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20 after pos.:80